

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/879,312A  
Source: IFW/6  
Date Processed by STIC: 3-4-05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 03/04/2005

PATENT APPLICATION: US/09/879,312A

TIME: 15:08:12

Input Set : A:\Hui27cpd.app

Output Set: N:\CRF4\03042005\I879312A.raw

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3 <110> APPLICANT: GLIMCHER, LAURIE H.
4     DOUHAN III, JOHN
6 <120> TITLE OF INVENTION: HUMAN C-MAF COMPOSITIONS AND METHODS OF USE THEREFOR
8 <130> FILE REFERENCE: HUI-027CPDV1
10 <140> CURRENT APPLICATION NUMBER: 09/879,312A
11 <141> CURRENT FILING DATE: 2001-06-12
13 <150> PRIOR APPLICATION NUMBER: 09/086,010
14 <151> PRIOR FILING DATE: 1998-05-27
16 <160> NUMBER OF SEQ ID NOS: 4
18 <170> SOFTWARE: PatentIn Ver. 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1203
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1203)
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32 1          5          10          15
34 ctg gcc atg gaa tat gtt aat gac ttc gat ctg atg aag ttt gaa gtg      96
35 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
36          20          25          30
38 aaa aag gaa ccg gtg gag acc gac cgc atc atc agc cag tgc ggc cgt      144
39 Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
40          35          40          45
42 ctc atc gcc ggg ggc tcg ctg tcc tcc acc ccc atg agc acg ccc tgc      192
43 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
44          50          55          60
46 agc tcg gtg ccc ccg tcc ccc agc ttc tcg gcg ccc agc ccg ggc tcg      240
47 Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
48 65          70          75          80
50 cga ggc gaa cag aag gcg cac ctg gaa gac tac tac tgg atg acc ggc      288
51 Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
52          85          90          95
54 tac ccg cag cag ctg aac ccc gag gcg ctg ggc ttc agc ccc gag gac      336
55 Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
56          100          105          110
58 gcg gtc gag gcg ctc atc agc aac agc cac cag ctc cgg ggc ggc ttc      384
59 Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe
60          115          120          125
62 gat ggc tat gcg cgc ggg gcg cag cag cta gcc gcg gcg gcc ggg gca      432

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63 Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Ala Gly Ala
64      130                      135                      140
66 ggt gcc ggc gcc tcc ttg ggc ggc agc ggc gag gag atg ggc ccc gcc      480
67 Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala
68 145                      150                      155                      160
70 gcc gcc gtg gtg tcc gcc gtg atc gcc gcg gcc gcc gcg cag agc ggc      528
71 Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Ala Ala Gln Ser Gly
72                      165                      170                      175
74 gcg ggc ccg cac tac cac cac cac cac cac gcc gcc ggc cac cac      576
75 Ala Gly Pro His Tyr His His His His His His Ala Ala Gly His His
76                      180                      185                      190
78 cac cac ccg acg gcc ggc gcg ccc ggc gcc gcg ggc agc gcg gcc gct      624
79 His His Pro Thr Ala Gly Ala Pro Gly Ala Ala Gly Ser Ala Ala Ala
80                      195                      200                      205
82 tcg gcc ggt ggc gct ggg ggc gcg ggc ggc ggt ggc ccg gcc agc gtt      672
83 Ser Ala Gly Gly Ala Gly Gly Ala Gly Gly Gly Gly Pro Ala Ser Val
84 210                      215                      220
86 ggg ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc      720
87 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala
88 225                      230                      235                      240
90 ggc gcc ctg cac ccg cac cac gcc gcc ggc ggc ctg cac ttc gac gac      768
91 Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp
92                      245                      250                      255
94 cgc ttc tcc gac gag cag ctg gtg acc atg tct gtg cgc gac tgg aac      816
95 Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn
96                      260                      265                      270
98 cgg cag ctg cgc ggg gtc agc aag gag gag gtg atc cgg ctg aag cag      864
99 Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln
100                      275                      280                      285
102 aag agg cgg acc ctg aaa aac cgc ggc tat gcc aag tcc tgc cgc ttc      912
103 Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe
104 290                      295                      300
106 aag agg gtg cag cag aga cac gtc ctg gag tgc gag aag aac cag ctg      960
107 Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu
108 305                      310                      315                      320
110 ctg cag caa gtc gac cac ctc aag cag gag atc tcc agg ctg gtg cgc      1008
111 Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg
112                      325                      330                      335
114 gag agg gac gcg tac aag gag aaa tac gag aag ttg gtg agc agc ggc      1056
115 Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly
116                      340                      345                      350
118 ttc cga gaa aac ggc tcg agc agc gac aac ccg tcc tct ccc gag ttt      1104
119 Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe
120                      355                      360                      365
122 ttc ata act gag ccc act cgc aag ttg gag cca tca gtg gga tac gcc      1152
123 Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala
124 370                      375                      380
126 aca ttt tgg aag ccc cag cat cgt gta ctt acc agt gtg ttc aca aaa      1200
127 Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys

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130 tga
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135 <211> LENGTH: 400
136 <212> TYPE: PRT
137 <213> ORGANISM: Homo sapiens
139 <400> SEQUENCE: 2
140 Met Ala Ser Glu Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro
141 1          5          10          15
143 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
144          20          25          30
146 Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
147          35          40          45
149 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
150          50          55          60
152 Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
153 65          70          75          80
155 Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
156          85          90          95
158 Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
159          100         105         110
161 Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe
162          115         120         125
164 Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Ala Gly Ala
165          130         135         140
167 Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala
168 145          150          155          160
170 Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Gln Ser Gly
171          165         170         175
173 Ala Gly Pro His Tyr His His His His His Ala Ala Gly His His
174          180         185         190
176 His His Pro Thr Ala Gly Ala Pro Gly Ala Ala Gly Ser Ala Ala Ala
177          195         200         205
179 Ser Ala Gly Gly Ala Gly Gly Ala Gly Gly Gly Gly Pro Ala Ser Val
180          210         215         220
182 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala
183 225          230          235          240
185 Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp
186          245         250         255
188 Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn
189          260         265         270
191 Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln
192          275         280         285
194 Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe
195          290         295         300
197 Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu
198 305          310          315          320
200 Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg
201          325         330         335

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203 Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly
204           340           345           350
206 Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe
207           355           360           365
209 Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala
210           370           375           380
212 Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys
213 385           390           395           400
218 <210> SEQ ID NO: 3
219 <211> LENGTH: 1119
220 <212> TYPE: DNA
221 <213> ORGANISM: Mus musculus
223 <220> FEATURE:
224 <221> NAME/KEY: CDS
225 <222> LOCATION: (1)..(1119)
227 <400> SEQUENCE: 3
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229 Met Ala Ser Glu Leu Ala Met Asn Asn Ser Asp Leu Pro Thr Ser Pro
230 1 5 10 15
232 ctg gcc atg gaa tat gtt aat gac ttc gat ctg atg aag ttt gaa gtg 96
233 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
234 20 25 30
236 aaa aag gaa ccg gtg gag acc gac cgc atc atc agc cag tgc ggc cgt 144
237 Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
238 35 40 45
240 ctc atc gcc ggg ggc tcg ctg tcc tcc acc ccc atg agc acg ccc tgc 192
241 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
242 50 55 60
244 agc tcg gtg ccc ccg tcc ccc agc ttc tcg gcg ccc agc ccg ggc tcg 240
245 Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
246 65 70 75 80
248 ggc agc gaa cag aag gcg cac ctg gaa gac tac tac tgg atg acc ggc 288
249 Gly Ser Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
250 85 90 95
252 tac ccg cag cag ctc aac ccg gag gcg ctg ggc ttc agc ccg gag gac 336
253 Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
254 100 105 110
256 gcg gtc gag gcg ctc atc agc aac agc cac cag ctc cag ggt ggc ttc 384
257 Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Gln Gly Gly Phe
258 115 120 125
260 gat ggc tat gcg cgg gga gcg cag cag ctg gcc gcg gca gcg ggg gcc 432
261 Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Gly Ala
262 130 135 140
264 ggc gcc ggc gcc tcc ctg ggc ggc agc ggc gag gag atg ggc ccc gcc 480
265 Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala
266 145 150 155 160
268 gcc gcc gtg gtg tcc gcc gtg atc gcc gcg gcc gcc gcg cag agc ggc 528
269 Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Ala Gln Ser Gly
270 165 170 175

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272 gcg gca ccc cac tac cat cac cac cac cac gcc gcg ggg cac cac 576
273 Ala Ala Pro His Tyr His His His His His His Ala Ala Gly His His
274      180      185      190
276 cac cat ccg acg gcc ggc gcc ccg gga acc gcg ggc ggc gcg tct tcc 624
277 His His Pro Thr Ala Gly Ala Pro Gly Thr Ala Gly Gly Ala Ser Ser
278      195      200      205
280 tct tcg aac ggc gcg ggt ggc gcg ggc ggc ggt ggc ccg gcc aac acc 672
281 Ser Ser Asn Gly Ala Gly Gly Ala Gly Gly Gly Gly Pro Ala Asn Thr
282      210      215      220
284 ggg ggc ggc ggc ggc gga gac ggc ggc ggg ggc acg gcg ggg gcg ggg 720
285 Gly Gly Gly Gly Gly Gly Asp Gly Gly Gly Gly Thr Ala Gly Ala Gly
286 225      230      235      240
288 ggc gcc ctt cac ccg cac cat tcc gcg ggc ggc ctg cac ttc gac gac 768
289 Gly Ala Leu His Pro His His Ser Ala Gly Gly Leu His Phe Asp Asp
290      245      250      255
292 cgc ttc tcg gac gag cag ttg gtg acc atg tcg gtg cgc gaa ctg aac 816
293 Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Glu Leu Asn
294      260      265      270
296 cgg cag ctg cgc ggg gtc agc aag gag gag gtg atc cga ctg aag cag 864
297 Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln
298      275      280      285
300 aag agg cgg acc ctg aaa aac cgc ggc tat gcc cag tcc tgc cgc ttc 912
301 Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Gln Ser Cys Arg Phe
302      290      295      300
304 aag agg gtg cag cag aga cac gtc ctg gag tcg gag aag aac cag ctg 960
305 Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu
306 305      310      315      320
308 ctg cag cag gta gac cac ctc aag cag gag atc tcc agg ctg gtg cgc 1008
309 Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg
310      325      330      335
312 gaa agg gac gcc tac aag gag aaa tac gag aag ctg gtg agc aac ggc 1056
313 Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Asn Gly
314      340      345      350
316 ttc cga gaa aac ggc tcg agc agc gac aac cct tcc tct ccc gaa ttt 1104
317 Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe
318      355      360      365
320 ttc atg tga gtg tga 1119
321 Phe Met
322      370
325 <210> SEQ ID NO: 4
326 <211> LENGTH: 370
327 <212> TYPE: PRT
328 <213> ORGANISM: Mus musculus
330 <400> SEQUENCE: 4
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332 1      5      10      15
334 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
335      20      25      30
337 Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg

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**VERIFICATION SUMMARY**

DATE: 03/04/2005

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